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ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
>US20040081980 SEQ ID NO:10                642 aa vs.
>US 10/674,636 SEQ ID NO:2                581 aa
scoring matrix: BLOSUM50, gap penalties: -12/-2
86.9% identity;                Global alignment score: 3612
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1



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          490          500          510          520          530          540
/tmp/s VPALITARYHRDAGAPVYFYEFRRHPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVM
      :
      :
SEQ    VPALITARYHRDAGAPVYFYEFRRHPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVM
      420          430          440          450          460          470

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          550          560          570          580          590          600
/tmp/s FEGATEEEKLLSRKMMKYWATFARTGNPNGNDLFLWPAYNLTEQYLQLDLNMSLGQRLKE
      :
      :
SEQ    FEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKE
      480          490          500          510          520          530

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          610          620          630          640
/tmp/s PRVEFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP
      :
      :
SEQ    PRVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP
      540          550          560          570          580

```